



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 142739

**TO: Nita M Minnifield**  
**Location: REM-3C01&3C18**  
**Art Unit: 1645**  
**Wednesday, January 19, 2005**

**Case Serial Number: 10/030231**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**Remsen 1-A-62**  
**Phone: 571-272-2524**

**maryjane.ruhl@uspto.gov**

### Search Notes

Examiner Minnifield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524

*Reviewed*  
*1-19-05*  
*mm*

142739

From: Chan, Christina  
Sent: Tuesday, January 18, 2005 10:18 AM  
To: Minnifield, Nita; STIC-Biotech/ChemLib  
Subject: RE: rush interference sequence search

**Please rush. Thanks Chris**

*Chris Chan*

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

CRFE

-----Original Message-----

From: Minnifield, Nita  
Sent: Friday, January 14, 2005 2:16 PM  
To: Chan, Christina  
Subject: rush interference sequence search

Christina, please approve, overdue AF amdt.

STIC

10/030231

Please do an interference sequence search on SEQ ID NO: 5, 6 and 7 of the above application.

Please provide a paper copy of the results.

Thanks,  
Minnifield  
71976  
Art Unit 1645  
Office REM-3C01  
Mailbox REM-3C18

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2005, 21:01:34 / Search time 17.333 Seconds  
(without alignments)  
153,042 Million cell updates/sec

Title: US-10-030-231-7  
Perfect score: 251  
Sequence: 1 HPHVCTSYGSKFCGTAGCTRYGCRNLHGRKLCFCHCSR 40

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
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2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	64	25.5	109 2	US-08-527-044-2 Sequence 2, Appl1
2	64	25.5	109 3	US-09-013-780-2 Sequence 2, Appl1
3	63	25.1	430 3	US-08-997-897-2 Sequence 2, Appl1
4	63	25.1	430 3	US-09-156-836B-2 Sequence 2, Appl1
5	62	24.7	97 4	US-09-673-395A-384 Sequence 384, App
6	62	24.7	97 4	US-09-673-395A-411 Sequence 411, App
7	61.5	24.5	1342 1	US-07-978-895-4 Sequence 9, Appl1
8	61.5	24.5	1342 2	US-08-484-438-9 Sequence 4, Appl1
9	61.5	24.5	1342 2	US-08-473-119-4 Sequence 4, Appl1
10	61.5	24.5	1342 2	US-08-475-352-4 Sequence 4, Appl1
11	61.5	24.5	1343 6	US-09-170-699-4 Patent No. 5183884
12	61.5	24.5	1343 6	US-09-491-522-5 Sequence 3523, A
13	61	24.3	1211 4	US-09-270-767-35232 Sequence 50449, A
14	60	23.9	129 4	US-09-270-767-50449 Sequence 10, Appl1
15	60	23.9	129 4	US-08-630-172-10 Sequence 10, Appl1
16	60	23.9	676 3	US-09-375-419-10 Sequence 1, Appl1
17	60	23.9	676 3	US-08-789-078-1 Sequence 1, Appl1
18	60	23.9	769 2	US-08-752-633-1 Sequence 45, Appl1
19	60	23.9	769 2	US-08-476-062A-45 Sequence 31, Appl1
20	60	23.9	769 2	US-07-728-215-31 Sequence 31, Appl1
21	60	23.9	769 3	US-08-938-085A-31 Sequence 31, Appl1
22	60	23.9	769 4	US-10-072-844-31 Sequence 31, Appl1
23	60	23.9	769 4	US-10-072-838-31 Sequence 31, Appl1
24	60	23.9	769 4	US-10-072-841A-31 Sequence 31, Appl1
25	60	23.9	769 4	US-10-219-631-31 Sequence 1, Appl1
26	60	23.9	769 5	PCT-US95-04866-1 Sequence 1, Appl1
27	60	23.9	769 5	PCT-US95-04866-1 Sequence 1, Appl1

28	60	23.9	769 5	PCT-US96-01314-45 Sequence 45, Appl1
29	59.5	23.7	147 4	US-09-252-991A-23465 Sequence 23465, A
30	59	23.5	969 4	US-09-321-987B-5 Sequence 5, Appl1
31	59	23.5	1205 5	US-09-491-522-11 Sequence 11, Appl1
32	59	23.5	2732 4	US-09-086-436-30 Sequence 30, Appl1
33	58.5	23.3	1345 2	US-08-977-767-3 Sequence 3, Appl1
34	58	23.1	70 3	US-09-188-930-131 Sequence 131, App
35	58	23.1	70 4	US-09-312-283C-131 Sequence 131, App
36	58	23.1	1064 4	US-09-270-767-45831 Sequence 45831, A
37	58	23.1	1193 2	US-08-400-159-10 Sequence 10, Appl1
38	58	23.1	1193 3	US-08-611-729A-10 Sequence 10, Appl1
39	58	23.1	1193 3	US-09-195-524-10 Sequence 10, Appl1
40	57.5	22.9	157 4	US-09-270-767-34570 Sequence 34570, A
41	57.5	22.9	157 4	US-09-270-767-49787 Sequence 49787, A
42	57.5	22.9	3460 3	US-09-334-220-1 Sequence 1, Appl1
43	57.5	22.9	3461 3	US-09-334-220-2 Sequence 2, Appl1
44	57	22.7	911 2	US-08-484-438-10 Sequence 10, Appl1
45	57	22.7	1058 2	US-08-484-438-8 Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-08-527-044-2  
Sequence 2, Application US/08527044  
Patent No. 5885568  
GENERAL INFORMATION:  
APPLICANT: BUNSTEAD, Janene Marilyn J.M.  
APPLICANT: TOMLEY, Fiona Margaret F.  
APPLICANT: DUNN, Patrick Paul James P.  
APPLICANT: VERMEULEN, Arnoldus Nicolaas A.N.  
TITLE OF INVENTION: Coccidiosis poultry vaccine  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Akzo No. 5885568el N.V.  
STREET: 1300 PICCARD DRIVE #206  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850-4373  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/527,044  
FILING DATE: 12-SEP-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 94202667.6  
FILING DATE: 16-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GORMLEY, MARY E.  
REGISTRATION NUMBER: 34,409  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-08-527-044-2  
Query Match 25.5% Score 64; DB 2; Length 109;  
Best Local Similarity 36.1%; Pred. No. 4;  
Matches 13; Conservative 4; Mismatches 15; Indels 4; Gaps 1;  
QY 5 CTSYCSKFCGTAGCTRYGCRNLHGRKLCFCHCSR 40  
DB 40 CSTYCSKFCGTAGCTRYGCRNLHGRKLCFCHCSR 71

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OM protein - protein search, using sw model

Run on: January 18, 2005, 21:05:30 ; Search time 84.333 Seconds  
(without alignments)  
171.363 Million cell updates/sec

Title: US-10-030-231-6

Perfect score: 252  
Sequence: 1 HSHACTSWCGKFCGTASCTHYLCRYLHPGKMCACVHCGR 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.5	28.0	479	US-10-408-765A-1798	Sequence 1798, Ap
2	70.5	28.0	666	US-10-108-260A-4771	Sequence 4771, Ap
3	67.5	26.8	2119	US-10-123-155-61	Sequence 61, Appl
4	67.5	26.8	2119	US-10-146-731-61	Sequence 61, Appl
5	67.5	26.8	2119	US-10-140-472-61	Sequence 61, Appl
6	67.5	26.8	2119	US-10-141-761-61	Sequence 61, Appl
7	67.5	26.8	2119	US-10-142-885-61	Sequence 61, Appl
8	67.5	26.8	2119	US-10-158-790-61	Sequence 61, Appl
9	67.5	26.8	2119	US-10-137-871-61	Sequence 61, Appl
10	67.5	26.8	2119	US-10-140-923-61	Sequence 61, Appl
11	67.5	26.8	2119	US-10-141-756-61	Sequence 61, Appl
12	67.5	26.8	2119	US-10-141-759-61	Sequence 61, Appl
13	67.5	26.8	2119	US-10-140-805-61	Sequence 61, Appl

14	67.5	26.8	2119	US-10-140-864-61	Sequence 61, Appl
15	67.5	26.8	2119	US-10-142-426-61	Sequence 61, Appl
16	66	26.2	1162	US-10-123-155-185	Sequence 185, Appl
17	66	26.2	1162	US-10-146-731-185	Sequence 185, Appl
18	66	26.2	1162	US-10-140-472-185	Sequence 185, Appl
19	66	26.2	1162	US-10-141-761-185	Sequence 185, Appl
20	66	26.2	1162	US-10-142-885-185	Sequence 185, Appl
21	66	26.2	1162	US-10-158-790-185	Sequence 185, Appl
22	66	26.2	1162	US-10-137-871-185	Sequence 185, Appl
23	66	26.2	1162	US-10-140-923-185	Sequence 185, Appl
24	66	26.2	1162	US-10-141-756-185	Sequence 185, Appl
25	66	26.2	1162	US-10-141-759-185	Sequence 185, Appl
26	66	26.2	1162	US-10-140-805-185	Sequence 185, Appl
27	66	26.2	1162	US-10-140-864-185	Sequence 185, Appl
28	66	26.2	1162	US-10-142-426-185	Sequence 185, Appl
29	64.5	25.6	1371	US-10-123-155-487	Sequence 487, Appl
30	64.5	25.6	1371	US-10-146-731-487	Sequence 487, Appl
31	64.5	25.6	1371	US-10-140-472-487	Sequence 487, Appl
32	64.5	25.6	1371	US-10-141-761-487	Sequence 487, Appl
33	64.5	25.6	1371	US-10-142-885-487	Sequence 487, Appl
34	64.5	25.6	1371	US-10-158-790-487	Sequence 487, Appl
35	64.5	25.6	1371	US-10-137-871-487	Sequence 487, Appl
36	64.5	25.6	1371	US-10-140-923-487	Sequence 487, Appl
37	64.5	25.6	1371	US-10-141-756-487	Sequence 487, Appl
38	64.5	25.6	1371	US-10-141-759-487	Sequence 487, Appl
39	64.5	25.6	1371	US-10-140-805-487	Sequence 487, Appl
40	64.5	25.6	1371	US-10-140-864-487	Sequence 487, Appl
41	64.5	25.6	1371	US-10-142-426-487	Sequence 487, Appl
42	64.5	25.6	3608	US-10-184-644-433	Sequence 433, Appl
43	64.5	25.6	3608	US-10-184-634-433	Sequence 433, Appl
44	64.5	25.6	7885	US-10-145-206-28	Sequence 28, Appl
45	64	25.4	188	US-09-808-602-109	Sequence 109, Appl

#### ALIGNMENTS

RESULT 1  
US-10-408-765A-1798  
Publication No. US20040101874A1  
GENERAL INFORMATION:  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Fahy, Boia D.  
APPLICANT: Zhang, Bing  
APPLICANT: Gibson, Bradford W.  
APPLICANT: Taylor, Steven W.  
APPLICANT: Warnock, Dale E.  
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
FILE REFERENCE: 660086.465  
CURRENT APPLICATION NUMBER: US/10/408,765A  
NUMBER OF SEQ ID NOS: 3077  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1798  
LENGTH: 479  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-408-765A-1798

Query Match 28.0% Score 70.5; DB 16; Length 479;  
Best Local Similarity 47.4% Pred. No. 15;  
Matches 18; Conservative 2; Mismatches 13; Indels 5; Gaps 4;

QY 7 SYWCGKFCGTA--SCTHYLCR--VILHPGKM--CACYHCGR 40  
DB 121 AVEGCK--CGKAFKCPSTVLCRHEVTHSGKRCCECKGCK 157

RESULT 2  
US-10-108-260A-4771

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 18, 2005, 21:01:34 ; Search time 17.333 Seconds  
(without alignments)  
153.042 Million cell updates/sec

Title: US-10-030-231-6  
Perfect score: 252  
Sequence: 1 HSHACTSWCKKFCGTASCTHYLCRVLHPGKMCACVHCSR 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCUTS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	27.0	281	4	US-09-248-796A-15282
2	62.5	24.8	55	4	US-09-716-129-139
3	62	24.6	2732	4	US-09-086-436-30
4	61.5	24.4	1248	3	US-08-882-046-6
5	61.5	24.4	1248	4	US-09-566-047-6
6	60	23.8	1497	4	US-09-060-854B-2
7	59.5	23.6	125	4	US-09-270-767-38974
8	59.5	23.6	125	4	US-09-270-767-54191
9	59.5	23.6	1055	3	US-09-214-278-2
10	59.5	23.6	1055	4	US-09-855-722-2
11	59.5	23.6	1065	2	US-08-400-159-8
12	59.5	23.6	1148	3	US-08-882-046-4
13	59.5	23.6	1148	4	US-09-566-047-4
14	59.5	23.6	1212	3	US-09-214-278-3
15	59.5	23.6	1212	4	US-09-855-722-3
16	59.5	23.6	1238	3	US-09-214-278-5
17	59.5	23.6	1238	4	US-09-855-722-5
18	59.5	23.6	1257	3	US-08-611-729A-8
19	59.5	23.6	1257	4	US-09-195-524-8
20	59.5	23.6	1652	4	US-09-627-650B-1
21	59.5	23.6	1652	4	US-09-627-650B-1
22	59.5	23.6	1917	4	US-09-436-063C-1
23	59.5	23.6	1917	4	US-09-627-650B-5
24	59.5	23.6	2508	4	US-09-436-063C-5
25	59.5	23.6	2508	4	US-09-627-650B-7
26	59.5	23.6	2544	4	US-09-436-063C-7
27	59.5	23.6	2544	4	US-09-627-650B-3

28	59.5	23.6	2601	4	US-09-627-650B-9	Sequence 9, App1
29	59.5	23.6	2601	4	US-09-436-063C-9	Sequence 9, App1
30	58.5	23.2	262	4	US-09-252-991A-22359	Sequence 22359, A
31	58.5	23.2	965	4	US-09-538-092-650	Sequence 650, App
32	58	23.0	3075	2	US-08-460-309-5	Sequence 5, App1
33	58	23.0	3075	2	US-08-125-077-5	Sequence 5, App1
34	57.5	22.8	148	4	US-09-270-767-47174	Sequence 47174, A
35	57.5	22.8	187	4	US-09-673-395A-148	Sequence 148, App
36	57	22.6	90	4	US-09-419-381-90	Sequence 90, App1
37	57	22.6	133	4	US-09-612-033B-6	Sequence 6, App1
38	57	22.6	180	4	US-09-612-033B-10	Sequence 10, App1
39	57	22.6	198	4	US-09-612-033B-8	Sequence 8, App1
40	57	22.6	398	4	US-09-612-033B-14	Sequence 14, App1
41	57	22.6	696	4	US-08-933-711B-7	Sequence 7, App1
42	56.5	22.4	112	4	US-09-621-976-5911	Sequence 5911, App
43	56	22.2	109	2	US-08-527-044-2	Sequence 2, App1
44	56	22.2	109	2	US-09-013-780-2	Sequence 2, App1
45	56	22.2	356	4	US-09-054-272-18	Sequence 18, App1

#### ALIGNMENTS

```

RESULT 1
US-09-248-796A-15282
; Sequence 15282, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15282
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15282

Query Match      27.0%; Score 68; DB 4; Length 281;
Best Local Similarity 27.6%; Pred. No. 3.3;
Matches 16; Conservative 4; Mismatches 12; Indels 26; Gaps 3;

QY      9 WCGKFE-----CGT-----ASCTHYLCRVLHPGKMCAC-----VHCSR 40
DB      164 WCGKLINEHNYLMPFGSCSMKNYKVASCVHSCCTYICHPGGHPICGATGPMKCHCGK 221

RESULT 2
US-09-716-129-139
; Sequence 139, Application US/09716129
; Patent No. 6632920
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P20251
; CURRENT APPLICATION NUMBER: US/09/716,129
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/076,053
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,057
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,052
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,054
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,051

```

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 18, 2005, 21:05:30 ; Search time 84.3333 Seconds  
(without alignments)  
171.363 Million cell updates/sec

Title: US-10-030-231-5

Perfect score: 199

Sequence: 1 HXHXCTXXCKKFCGTACTXXCXRLHXGXCKXCHCSR 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66.5	33.4	479	16	US-10-408-765A-1798 Sequence 1798, App
2	66.5	33.4	666	15	US-10-108-260A-4771 Sequence 4771, App
3	66	33.2	2095	14	US-10-184-644-161 Sequence 161, App
4	66	33.2	2095	14	US-10-184-644-161 Sequence 161, App
5	66	33.2	2095	14	US-10-063-685-15 Sequence 35, Appl
6	65	32.7	2089	14	US-10-123-155-497 Sequence 497, App
7	65	32.7	2089	14	US-10-146-731-497 Sequence 497, App
8	65	32.7	2089	14	US-10-140-472-497 Sequence 497, App
9	65	32.7	2089	14	US-10-141-761-497 Sequence 497, App
10	65	32.7	2089	14	US-10-142-885-497 Sequence 497, App
11	65	32.7	2089	14	US-10-158-790-497 Sequence 497, App
12	65	32.7	2089	14	US-10-137-871-497 Sequence 497, App
13	65	32.7	2089	14	US-10-140-923-497 Sequence 497, App

14	65	32.7	2089	14	US-10-141-756-497 Sequence 497, App
15	65	32.7	2089	14	US-10-141-759-497 Sequence 497, App
16	65	32.7	2089	14	US-10-140-805-497 Sequence 497, App
17	65	32.7	2089	14	US-10-140-864-497 Sequence 497, App
18	65	32.7	2089	15	US-10-142-426-497 Sequence 497, App
19	63	31.7	2732	10	US-09-086-436-30 Sequence 30, Appl
20	63	31.7	2732	16	US-10-753-991-30 Sequence 30, Appl
21	63	31.7	2870	14	US-10-184-644-473 Sequence 473, App
22	63	31.7	3244	14	US-10-184-644-473 Sequence 473, App
23	63	31.7	3244	14	US-10-184-644-471 Sequence 571, App
24	63	31.7	3244	14	US-10-184-644-471 Sequence 571, App
25	63	31.7	3608	14	US-10-184-644-433 Sequence 433, App
26	63	31.7	3608	14	US-10-184-644-433 Sequence 433, App
27	62	31.2	1497	9	US-09-060-854B-2 Sequence 2, Appl1
28	62	31.2	3907	14	US-10-029-217A-24 Sequence 24, Appl
29	61.5	30.9	3479	14	US-10-123-155-123 Sequence 123, App
30	61.5	30.9	3479	14	US-10-146-721-123 Sequence 123, App
31	61.5	30.9	3479	14	US-10-140-472-123 Sequence 123, App
32	61.5	30.9	3479	14	US-10-141-761-123 Sequence 123, App
33	61.5	30.9	3479	14	US-10-142-885-123 Sequence 123, App
34	61.5	30.9	3479	14	US-10-158-790-123 Sequence 123, App
35	61.5	30.9	3479	14	US-10-137-871-123 Sequence 123, App
36	61.5	30.9	3479	14	US-10-140-923-123 Sequence 123, App
37	61.5	30.9	3479	14	US-10-141-756-123 Sequence 123, App
38	61.5	30.9	3479	14	US-10-141-759-123 Sequence 123, App
39	61.5	30.9	3479	14	US-10-140-805-123 Sequence 123, App
40	61.5	30.9	3479	14	US-10-140-864-123 Sequence 123, App
41	61.5	30.9	3479	15	US-10-142-426-123 Sequence 123, App
42	61.5	30.9	4679	9	US-09-804-898-2 Sequence 2, Appl1
43	61	30.7	636	14	US-10-123-155-507 Sequence 507, App
44	61	30.7	636	14	US-10-146-721-507 Sequence 507, App
45	61	30.7	636	14	US-10-140-472-507 Sequence 507, App

## ALIGNMENTS

RESULT 1  
US-10-408-765A-1798  
; Sequence 1798, Application US/10408765A  
; Publication No. US20040101674A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghost, Soumitra S.  
; APPLICANT: Fahy, Bojin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1798  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1798

Query Match 33.4% Score 66.5; DB 16; Length 479;  
Best Local Similarity 42.1%; Pred. No. 2.5;  
Matches 16; Conservative 2; Mismatches 15; Indels 5; Gaps 4;

QY 7 SYXCKKFCGT-XCTYXCR-XLHXGX-CKXCHCSR 40  
Db 121 AVECTK-CGKAFKCPSYLCHRHVTHSGKPCCKCCK 157

RESULT 2  
US-10-108-260A-4771

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: January 18, 2005, 21:01:34 ; Search time 17.333 Seconds  
(without alignments)  
153.042 Million cell updates/sec

Title: US-10-030-231-5  
Perfect score: 199  
Sequence: 1 HXHCSTSYCKKFCGTAACXYYXCRXHXGKXCKXCHCSR 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTS COMB pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1 pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	31.7	2732	4	US-09-086-436-30 Sequence 30, Appl
2	62	31.2	1497	4	US-09-060-854B-2 Sequence 2, Appl
3	57	28.6	109	2	US-08-527-044-2 Sequence 2, Appl
4	57	28.6	109	3	US-09-013-780-2 Sequence 2, Appl
5	55	27.6	430	3	US-08-997-897-2 Sequence 2, Appl
6	55	27.6	430	3	US-09-156-836B-2 Sequence 2, Appl
7	55	27.6	1461	4	US-10-142-231-86 Sequence 86, Appl
8	55	27.6	2088	4	US-09-548-372D-13 Sequence 13, Appl
9	55	27.6	2088	4	US-09-548-372D-13 Sequence 13, Appl
10	55	27.6	2088	4	US-09-548-372D-13 Sequence 13, Appl
11	55	27.6	2088	4	US-09-548-372D-13 Sequence 13, Appl
12	55	27.6	2088	4	US-09-548-372D-13 Sequence 13, Appl
13	55	27.6	2088	4	US-09-548-372D-13 Sequence 13, Appl
14	54.5	27.4	1917	4	US-09-548-366F-13 Sequence 13, Appl
15	54.5	27.4	1917	4	US-09-548-366F-13 Sequence 13, Appl
16	54	27.1	1917	4	US-09-548-366F-13 Sequence 13, Appl
17	53.5	26.9	281	4	US-09-352-991A-29199 Sequence 29199, A
18	53.5	26.9	2508	4	US-09-716-129-139 Sequence 139, A
19	53.5	26.9	2508	4	US-09-527-650B-7 Sequence 7, Appl
20	53.5	26.9	2544	4	US-09-436-063C-7 Sequence 7, Appl
21	53.5	26.9	2544	4	US-09-627-650B-3 Sequence 3, Appl
22	53.5	26.9	2544	4	US-09-436-063C-3 Sequence 3, Appl
23	53.5	26.9	2601	4	US-09-627-650B-9 Sequence 9, Appl
24	53	26.6	1388	4	US-09-436-063C-9 Sequence 9, Appl
25	53	26.6	1417	3	US-08-900-230-3 Sequence 3, Appl
26	51.5	25.9	908	4	US-08-714-741-44 Sequence 44, Appl
27	51.5	25.9	2211	3	US-09-738-884-1 Sequence 1, Appl

28	51.5	25.9	2211	4	US-10-096-961A-1 Sequence 1, Appl
29	50	25.1	90	4	US-09-419-381-90 Sequence 90, Appl
30	50	25.1	143	3	US-08-990-823-112 Sequence 112, App
31	50	25.1	143	4	US-09-477-135A-112 Sequence 112, App
32	50	25.1	1652	4	US-09-627-650B-1 Sequence 1, Appl
33	50	25.1	1652	4	US-09-627-650B-1 Sequence 1, Appl
34	49.5	24.9	1128	4	US-09-627-650B-11 Sequence 11, Appl
35	49.5	24.9	1128	4	US-09-627-650B-11 Sequence 11, Appl
36	49	24.6	379	1	US-08-468-847B-11 Sequence 11, Appl
37	49	24.6	379	4	US-09-142-569-2 Sequence 2, Appl
38	49	24.6	379	4	US-09-495-448-2 Sequence 2, Appl
39	49	24.6	717	4	US-09-644-460-37 Sequence 37, Appl
40	48.5	24.4	518	4	US-09-881-578A-4 Sequence 4, Appl
41	48	24.1	414	4	US-08-630-915A-37 Sequence 37, Appl
42	48	24.1	1400	3	US-08-630-915A-37 Sequence 37, Appl
43	48	24.1	1400	4	US-09-879-957-37 Sequence 37, Appl
44	47.5	23.9	138	4	US-09-270-767-39484 Sequence 39484, A
45	47.5	23.9	138	4	US-09-270-767-54701 Sequence 54701, A

## ALIGNMENTS

```

RESULT 1
US-09-086-436-30
Sequence 30, Application US/09086436
Patent No. 6703485
GENERAL INFORMATION:
APPLICANT: Kandell, Eric R.
APPLICANT: Santoro, Bina
APPLICANT: Bartsch, Dusan
APPLICANT: Siegelbaum, Steven
APPLICANT: Tibbs, Gareth
APPLICANT: Grant, Seth
TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
FILE REFERENCE: 0575/54806-A
CURRENT APPLICATION NUMBER: US/09/086,436
CURRENT FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 2732
TYPE: PRT
ORGANISM: Murine
US-09-086-436-30

Query Match          31.7%; Score 63; DB 4; Length 2732;
Best Local Similarity 31.4%; Pred. No. 9.2;
Matches 11; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY      5 CTSYXCKKFCGTAACXYYXCRXHXGKXCKXCHCS 39
DB      2425 CCTCGACGCTCTCTGCCCCCATGAGTCTCCACT 2459

RESULT 2
US-09-060-854B-2
Sequence 2, Application US/09060854B
Patent No. 6642011
GENERAL INFORMATION:
APPLICANT: Estell, David Aaron
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011-H
FILE REFERENCE: GC532
CURRENT APPLICATION NUMBER: US/09/060,854B
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1497
TYPE: PRT

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